RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:	10/539,535A
Source:	IFWP
Date Processed by STIC:	10/12/2006

ENTERED



IFWP

RAW SEQUENCE LISTING DATE: 10/12/2006
PATENT APPLICATION: US/10/539,535A TIME: 09:28:07

Input Set : A:\41384.txt

Output Set: N:\CRF4\10122006\J539535A.raw

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      5 <120> TITLE OF INVENTION: Use of the Multifunctional Transcription Factor
Yin Yang 1 and
      6
              Variants Thereof for Treating Illnesses, Especially Type I
      7
              Diabetes
      9 <130> FILE REFERENCE: 30572/41384
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/539,535A
C--> 11 <141> CURRENT FILING DATE: 2005-06-17
     11 <150> PRIOR APPLICATION NUMBER: PCT/EP03/014762
     12 <151> PRIOR FILING DATE: 2003-12-19
     14 <150> PRIOR APPLICATION NUMBER: DE 102 61 650.7
     15 <151> PRIOR FILING DATE: 2002-12-20
     17 <160> NUMBER OF SEQ ID NOS: 232
    19 <170> SOFTWARE: PatentIn version 3.3
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    32 <222> LOCATION: (73)..(1125)
    33 <223> OTHER INFORMATION: YY1 (BB/OK)
    35 <220> FEATURE:
    36 <221> NAME/KEY: misc_feature
    37 <222> LOCATION: (955)..(1125)
    38 <223> OTHER INFORMATION: Zinc finger
    40 <220> FEATURE:
    41 <221> NAME/KEY: Intron
    42 <222> LOCATION: (1126)..(1758)
    44 <220> FEATURE:
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    46 <222> LOCATION: (1759)..(1917)
    47 <223> OTHER INFORMATION: Zinc finger
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    51 <222> LOCATION: (1759)..(1938)
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Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly

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65 acc atc ccg gtg gag act atc gag acc acg gtg gtg gtg gag gag gag gag 66 Thr Ile Pro Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu 67 30					
65 acc atc ccg gtg gag act atc gag acc acg gtg gtg gtg gag gag gag gag 66 Thr I1e Pro Val Glu Thr I1e Glu Thr Thr Val Val Gly Glu Glu Glu 67 30 35 40 45 69 gac gac gac gac gac gag gat ggt ggc ggc gag ac cac ggt ggc 70 Asp Asp Asp Glu Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly Gly 71 50 50 55 60 70 75 70 Asp Asp Glu Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly					Val Glu
67 300 35 40 45 69 gac gac gac gac gac gac gat ggt ggc ggc ggc gac cac ggt ggc 70 Asp Asp Asp Asp Glu Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly 71 50 65 60 73 ggg ggc ggc cac ggc acc cac cac cac cac	65 acc atc ccg	gtg gag act at	c gag acc acg	gtg gtg ggc gag	gag gag 207
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70 Asp Asp Asp Glu Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly 71					
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74 Gly Gly Gly His Gly His Ala Gly His	71	50	55		60
75 77 cac cac ccg ccc atg atc gcg ctg cag ccg ctg gtc acc gac gac ccg 351 78 His His Pro Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro 79 80 81 acc caa gtg cac cac cac cac agag gtg att ctg gtg cag acg gg gag 399 81 acc caa gtg cac cac cac cac agag gtg att ctg gtg cag acg gg gag 399 82 Thr Gln Val His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu 83 95 100 105 85 gag gta gtg gg gg gg gac gac tcg gac gg gg gg gg gg gg gg gg gg gac gac					
77 cac cac ccg ccc atg atc gcg ctg cag ccg ctg gtc acc gac gac ccg 78 His His Pro Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro 80 80 80 81 80 80 81 80 80 80			=		HIS HIS
78 His His Pro Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro 90 80 85 90 85 90 90 85 90 85 90 85 90 85 90 85 90 85 90 85 90 85 90 85 90 85 90 85 90 90 85 90 90 85 90 90 85 90 90 85 90 90 90 85 90 90 90 90 90 90 90 90 90 90 90 90 90			· -	· -	gac ccg 351
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83 95 100 105					
86 Glu Val Val Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly 87 110					Alg Glu
87 110					
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90 Phe Glu Asp Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp 91					
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94 Asp Asp Tyr Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys 95	91	130	135	_	140
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97 agc ggt ggc ggg tct tcg tcg ggc ggc ggc cgc gtt aag aag ggc ggc 591 98 Ser Gly Gly Gly Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly 99 160 165 170 101 ggc aag aag agc ggc aag aag agt tac ctg ggc agc ggg gcc ggc gcg 639 102 Gly Lys Lys Ser Gly Lys Lys Ser Tyr Leu Gly Ser Gly Ala Gly Ala 103 175 180 185 105 gcg ggc ggt ggc ggc gcc gac ccg ggt aat aag aag tgg gaa cag aag 687 106 Ala Gly Gly Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys 107 190 195 200 205 109 cag gtg cag atc aag acc ctg gag ggc gag ttc tcg gtc acc atg tgg 735 110 Gln Val Gln Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp 111 210 210 215 220 113 tct tca gat gaa aaa aaa gat att gac cat gaa aca gtg gtt gaa gag 783 114 Ser Ser Asp Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu 115 225 230 235 117 cag atc att ggg gag acc tca cct cct gat tat tct gaa tat atg aca 831 118 Gln Ile Ile Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr 119 240 245 250 121 ggc aag aaa ctc cct cct gga ggg ata cct ggc att gac ctc tca gac 879 122 Gly Lys Lys Lys Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp					GIA TAR
98 Ser Gly Gly Gly Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly 99					ggc ggc 591
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107 190					
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taran da antara da a					
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127 270 275 280 285	
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130 Glu Asp Asp Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr	
131 290 295 300	
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134 Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His	
135 305 310 315	
137 ggt ccc aga gtc cac gtc tgt gca gaa tgt ggc aaa gcg ttc gtt gag	1071
138 Gly Pro Arg Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu	
139 320 325 330	
141 agc tca aag cta aaa cga cac cag ctg gtt cat act gga gaa aag ccc	1119
142 Ser Ser Lys Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro	
143 335 340 345	
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146 Phe Gln	11/5
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228 Glu Asp Asp Glu Asp Gly Gly Gly Asp His Gly Gly Gly Gly Gly
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268 Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp Ser Ser Asp
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RAW SEQUENCE LISTING DATE: 10/12/2006
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292 Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His Gly Pro Arg 293 305 315 296 Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu Ser Ser Lys 297 325 330 300 Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro Phe Gln Cys 301 340 345 304 Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe Asn Leu Arg 305 360 365 308 Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val Cys Pro Phe 309 370 375 380 312 Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu Lys Ser His 390 395 316 Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln 317 320 <210> SEQ ID NO: 3 321 <211> LENGTH: 2256 322 <212> TYPE: DNA 323 <213> ORGANISM: Rattus norv. 325 <220> FEATURE: 326 <221> NAME/KEY: Promoter 327 <222> LOCATION: (1)..(72) 329 <220> FEATURE: 330 <221> NAME/KEY: CDS 331 <222> LOCATION: (73)..(1125) 332 <223> OTHER INFORMATION: YY1 (SHR) 334 <220> FEATURE: 335 <221> NAME/KEY: misc feature 336 <222> LOCATION: (955)..(1125) 337 <223> OTHER INFORMATION: Zinc finger 339 <220> FEATURE: 340 <221> NAME/KEY: Intron 341 <222> LOCATION: (1126)..(1758) 343 <220> FEATURE: 344 <221> NAME/KEY: misc feature 345 <222> LOCATION: (1759)..(1917) 346 <223> OTHER INFORMATION: Zinc finger 348 <220> FEATURE: 349 <221> NAME/KEY: CDS 350 <222> LOCATION: (1759)..(1938) 351 <223> OTHER INFORMATION: YY1 (SHR) 353 <400> SEQUENCE: 3 354 cegeeteete geeegeeete eegeageeea ggageegagg etgeegegge egtggeggeg 60 356 gageceteag ee atg gee teg gge gae ace ete tae att gee aeg gae gge 111 357 Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly 358 360 tcg gag atg cca gcc gag atc gtg gaa ctg cat gag att gag gtg gag 159 361 Ser Glu Met Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu 20 364 acc atc ccg gtg gag act atc gag acc acg gtg gtg ggc gag gag 207

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/539,535A

DATE: 10/12/2006 TIME: 09:28:08

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